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RAW SEQUENCE LISTING DATE: 04/17/2002
PATENT APPLICATION: US/09/909,775 TIME: 14:08:36

Input Set : A:\Sequence Listing.txt
Output Set: N:\CRF3\04172002\I909775.raw

<110> APPLICANT: Genzyme Corporation
Schiavi, Susan
Madden, Stephen L.
Manavalan, Parthasarathy
Levine, Michael
Jan de Beur, Suzanne
<120> TITLE OF INVENTION: PHOSPHATONIN-RELATED GENE AND METHODS OF USE THEREOF
<130> FILE REFERENCE: GZ 2065.23
<140> CURRENT APPLICATION NUMBER: US 09/909,775
<141> CURRENT FILING DATE: 2001-07-19
<150> PRIOR APPLICATION NUMBER: US 60/219,365
<151> PRIOR FILING DATE: 2000-07-19
<150> PRIOR APPLICATION NUMBER: US 60/261,438
<151> PRIOR FILING DATE: 2001-01-12
<160> NUMBER OF SEQ ID NOS: 2
<170> SOFTWARE: FastSEQ for Windows Version 4.0
<210> SEQ ID NO: 1
<211> LENGTH: 2839
<212> TYPE: DNA
<213> ORGANISM: Homo sapien
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (257)...(1297)
<400> SEQUENCE: 1

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gactggagtt tgggggaaga aactctcctg cgccccagaa gatttcttcc tcggcgaagg 180
gacagcgaaa gatgagggtg gcaggaagag aaggcgcttt ctgtctgccg gggtcgcagc 240
gcgagagggc agtgcc atg ttc ctc tcc atc cta gtg gcg ctg tgc ctg tgg 292
                  Met Phe Leu Ser Ile Leu Val Ala Leu Cys Leu Trp
                   1               5                  10
ctg cac ctg gcg ctg ggc gtg cgc ggc gcg ccc tgc gag gcg gtg cgc   340
Leu His Leu Ala Leu Gly Val Arg Gly Ala Pro Cys Glu Ala Val Arg
          15                  20                  25
atc cct atg tgc cgg cac atg ccc tgg aac atc acg cgg atg ccc aac   388
Ile Pro Met Cys Arg His Met Pro Trp Asn Ile Thr Arg Met Pro Asn
      30                  35                  40
cac ctg cac cac agc acg cag gag aac gcc atc ctg gcc atc gag cag   436
His Leu His His Ser Thr Gln Glu Asn Ala Ile Leu Ala Ile Glu Gln
  45                  50                  55                  60
tac gag gag ctg gtg gac gtg aac tgc agc gcc gtg ctg cgc ttc ttc   484
Tyr Glu Glu Leu Val Asp Val Asn Cys Ser Ala Val Leu Arg Phe Phe
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61                  65                  70                  75
63 ttc tgt gcc atg tac gcg ccc att tgc acc ctg gag ttc ctg cac gac   532
64 Phe Cys Ala Met Tyr Ala Pro Ile Cys Thr Leu Glu Phe Leu His Asp
65              80                  85                  90
67 cct atc aag ccg tgc aag tcg gtg tgc caa cgc gcg cgc gac gac tgc   580
68 Pro Ile Lys Pro Cys Lys Ser Val Cys Gln Arg Ala Arg Asp Asp Cys
69          95                  100                 105
71 gag ccc ctc atg aag atg tac aac cac agc tgg ccc gaa agc ctg gcc   628
72 Glu Pro Leu Met Lys Met Tyr Asn His Ser Trp Pro Glu Ser Leu Ala
73      110                 115                 120
75 tgc gac gag ctg cct gtc tat gac cgt ggc gtg tgc att tcg cct gaa   676
76 Cys Asp Glu Leu Pro Val Tyr Asp Arg Gly Val Cys Ile Ser Pro Glu
77 125                 130                 135                 140
79 gcc atc gtc acg gac ctc ccg gag gat gtt aag tgg ata gac atc aca   724
80 Ala Ile Val Thr Asp Leu Pro Glu Asp Val Lys Trp Ile Asp Ile Thr
81                  145                 150                 155
83 cca gac atg atg gta cag gaa agg cct ctt gat gtt gac tgt aaa cgc   772
84 Pro Asp Met Met Val Gln Glu Arg Pro Leu Asp Val Asp Cys Lys Arg
85              160                 165                 170
87 cta agc ccc gat cgg tgc aag tgt aaa aag gtg aag cca act ttg gca   820
88 Leu Ser Pro Asp Arg Cys Lys Cys Lys Lys Val Lys Pro Thr Leu Ala
89          175                 180                 185
91 acg tat ctc agc aaa aac tac agc tat gtt att cat gcc aaa ata aaa   868
92 Thr Tyr Leu Ser Lys Asn Tyr Ser Tyr Val Ile His Ala Lys Ile Lys
93      190                 195                 200
95 gct gtg cag agg agt ggc tgc aat gag gtc aca acg gtg gtg gat gta   916
96 Ala Val Gln Arg Ser Gly Cys Asn Glu Val Thr Thr Val Val Asp Val
97 205                 210                 215                 220
99 aaa gag atc ttc aag tcc tca tca ccc atc cct cga act caa gtc ccg   964
100 Lys Glu Ile Phe Lys Ser Ser Ser Pro Ile Pro Arg Thr Gln Val Pro
101                 225                 230                 235
103 ctc att aca aat tct tct tgc cag tgt cca cac atc ctg ccc cat caa  1012
104 Leu Ile Thr Asn Ser Ser Cys Gln Cys Pro His Ile Leu Pro His Gln
105             240                 245                 250
107 gat gtt ctc atc atg tgt tac gag tgg cgt tca agg atg atg ctt ctt  1060
108 Asp Val Leu Ile Met Cys Tyr Glu Trp Arg Ser Arg Met Met Leu Leu
109         255                 260                 265
111 gaa aat tgc tta gtt gaa aaa tgg aga gat cag ctt agt aaa aga tcc  1108
112 Glu Asn Cys Leu Val Glu Lys Trp Arg Asp Gln Leu Ser Lys Arg Ser
113     270                 275                 280
115 ata cag tgg gaa gag agg ctg cag gaa cag cgg aga aca gtt cag gac  1156
116 Ile Gln Trp Glu Glu Arg Leu Gln Glu Gln Arg Arg Thr Val Gln Asp
117 285                 290                 295                 300
119 aag aag aaa aca gcc ggg cgc acc agt cgt agt aat ccc ccc aaa cca  1204
120 Lys Lys Lys Thr Ala Gly Arg Thr Ser Arg Ser Asn Pro Pro Lys Pro
121                 305                 310                 315
123 aag gga aag cct cct gct ccc aaa cca gcc agt ccc aag aag aac att  1252
124 Lys Gly Lys Pro Pro Ala Pro Lys Pro Ala Ser Pro Lys Lys Asn Ile
125             320                 325                 330
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127 aaa act agg agt gcc cag aag aga aca aac ccg aaa aga gtg tga       1297
128 Lys Thr Arg Ser Ala Gln Lys Arg Thr Asn Pro Lys Arg Val  *
129         335                 340                 345
131 gctaactagt ttccaaagcg gagacttccg acttccttac aggatgaggc tgggcattgc 1357
132 ctgggacagc ctatgtaagg ccatgtgccc cttgccctaa caactcactg cagtgctctt 1417
133 catagacaca tcttgcagca tttttcttaa ggctatgctt cagtttttct ttgtaagcca 1477
134 tcacaagcca tagtggtagg tttgcccttt ggtacagaag gtgagttaaa gctggtggaa 1537
135 aaggcttatt gcattgcatt cagagtaacc tgtgtgcata ctctagaaga gtagggaaaa 1597
136 taatgcttgt tacaattcga cctaatatgt gcattgtaaa ataaatgcca tatttcaaac 1657
137 aaaacacgta atttttttac agtatgtttt attacctttt gatatctgtt gttgcaatgt 1717
138 tagtgatgtt ttaaaatgtg atgaaaatat aatgttttta agaaggaaca gtagtggaat 1777
139 gaatgttaaa agatctttat gtgtttatgg tctgcagaag gatttttgtg atgaaagggg 1837
140 atttttgaa aaattagaga agtagcatat ggaaaattat aatgtgtttt tttaccaatg 1897
141 acttcagttt ctgtttttag ctagaaactt aaaaacaaaa ataataataa agaaaaataa 1957
142 ataaaaagga gaggcagaca atgtctggat tcctgttttt tggttacctg atttccatga 2017
143 tcatgatgct tcttgtcaac accctcttaa gcagcaccag aaacagtgag tttgtctgta 2077
144 ccattaggag ttaggtacta attagttggc taatgctcaa gtattttata cccacaagag 2137
145 aggtatgtca ctcatcttac ttcccaggac atccaccctg agaataattt gacaagctta 2197
146 aaaatggcct tcatgtgagt gccaaatttt gtttttcttc atttaaatat tttctttgcc 2257
147 taaatacatg tgagaggagt taaatataaa tgtacagaga ggaaagttga gttccacctc 2317
148 tgaaatgaga attacttgac agttgggata ctttaatcag aaaaaaagaa cttatttgca 2377
149 gcattttatc aacaaatttc ataattgtgg acaattggag gcatttattt taaaaaacaa 2437
150 ttttattggc cttttgctaa cacagtaagc atgtatttta taaggcattc aataaatgca 2497
151 caacgcccaa aggaaataaa atcctatcta atcctactct ccactacaca gaggtaatca 2557
152 ctattagtat tttggcatat tattctccag gtgtttgctt atgcacttat aaaatgattt 2617
153 gaacaaataa aactaggaac ctgtatacat gtgtttcata acctgcctcc tttgcttggc 2677
154 cctttattga gataagtttt cctgtcaaga aagcagaaac catctcattt ctaacagctg 2737
155 tgttatattc catagtatgc attactcaac aaactgttgt gctattggat acttaggtgg 2797
156 tttcttcact gacaatactg aataaacatc tcaccggaat tc                    2839
158 <210> SEQ ID NO: 2
159 <211> LENGTH: 346
160 <212> TYPE: PRT
161 <213> ORGANISM: Homo sapien
163 <400> SEQUENCE: 2
164 Met Phe Leu Ser Ile Leu Val Ala Leu Cys Leu Trp Leu His Leu Ala
165  1               5                  10                  15
166 Leu Gly Val Arg Gly Ala Pro Cys Glu Ala Val Arg Ile Pro Met Cys
167             20                  25                  30
168 Arg His Met Pro Trp Asn Ile Thr Arg Met Pro Asn His Leu His His
169         35                  40                  45
170 Ser Thr Gln Glu Asn Ala Ile Leu Ala Ile Glu Gln Tyr Glu Glu Leu
171     50                  55                  60
172 Val Asp Val Asn Cys Ser Ala Val Leu Arg Phe Phe Phe Cys Ala Met
173 65                  70                  75                  80
174 Tyr Ala Pro Ile Cys Thr Leu Glu Phe Leu His Asp Pro Ile Lys Pro
175                 85                  90                  95
176 Cys Lys Ser Val Cys Gln Arg Ala Arg Asp Asp Cys Glu Pro Leu Met
177             100                 105                 110
178 Lys Met Tyr Asn His Ser Trp Pro Glu Ser Leu Ala Cys Asp Glu Leu
```

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```
179          115                 120                 125
180 Pro Val Tyr Asp Arg Gly Val Cys Ile Ser Pro Glu Ala Ile Val Thr
181      130                 135                 140
182 Asp Leu Pro Glu Asp Val Lys Trp Ile Asp Ile Thr Pro Asp Met Met
183 145                 150                 155                 160
184 Val Gln Glu Arg Pro Leu Asp Val Asp Cys Lys Arg Leu Ser Pro Asp
185                 165                 170                 175
186 Arg Cys Lys Cys Lys Lys Val Lys Pro Thr Leu Ala Thr Tyr Leu Ser
187             180                 185                 190
188 Lys Asn Tyr Ser Tyr Val Ile His Ala Lys Ile Lys Ala Val Gln Arg
189          195                 200                 205
190 Ser Gly Cys Asn Glu Val Thr Thr Val Val Asp Val Lys Glu Ile Phe
191      210                 215                 220
192 Lys Ser Ser Ser Pro Ile Pro Arg Thr Gln Val Pro Leu Ile Thr Asn
193 225                 230                 235                 240
194 Ser Ser Cys Gln Cys Pro His Ile Leu Pro His Gln Asp Val Leu Ile
195                 245                 250                 255
196 Met Cys Tyr Glu Trp Arg Ser Arg Met Met Leu Leu Glu Asn Cys Leu
197             260                 265                 270
198 Val Glu Lys Trp Arg Asp Gln Leu Ser Lys Arg Ser Ile Gln Trp Glu
199          275                 280                 285
200 Glu Arg Leu Gln Glu Gln Arg Arg Thr Val Gln Asp Lys Lys Lys Thr
201      290                 295                 300
202 Ala Gly Arg Thr Ser Arg Ser Asn Pro Pro Lys Pro Lys Gly Lys Pro
203 305                 310                 315                 320
204 Pro Ala Pro Lys Pro Ala Ser Pro Lys Lys Asn Ile Lys Thr Arg Ser
205                 325                 330                 335
206 Ala Gln Lys Arg Thr Asn Pro Lys Arg Val
207             340                 345
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